



SEQUENCE LISTING

<110> CHANG, Y-H
VETRO, J.A.
MICKA, W.S.

<120> DOMINANT NEGATIVE VARIANTS OF METHIONINE AMINOPEPTIDASE 2 ("METAP2") AND CLINICAL USES THEREFOR

<130> 2790/66153/8007

<140> 10/712,359
<141> 2003-11-13

<150> 09/943,123
<151> 2001-08-30

<160> 26

<170> PatentIn Ver. 3.2

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<212> PRT
<213> Homo Sapiens

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Lys Lys Lys Lys Lys Lys
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<212> PRT
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Lys Lys Lys Lys Lys Lys
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Ser Lys Gly Pro
35 40 45

Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
50 55 60

Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
65 70 75 80

Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Gln Tyr
325 330 335

Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Glu Ala
340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
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20

25

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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala
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Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr

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330

335

Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Leu
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Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
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Asp Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys
35 40 45

Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
50 55 60

Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
65 70 75 80

Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
85 90 95

Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
100 105 110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
115 120 125

Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
130 135 140

Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
145 150 155 160

Gly Xaa Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala Xaa Phe Thr
165 170 175

Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
180 185 190

Val Xaa Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Xaa Ser Ala Phe
195 200 205

Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
210 215 220

Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
225 230 235 240

Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
245 250 255

Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Xaa Cys
260 265 270

Gly Xaa Ser Ile Ala Pro Tyr Arg Xaa Xaa Gly Gly Lys Ser Val Pro
275 280 285

Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
290 295 300

Ala Ile Xaa Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
305 310 315 320

Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
325 330 335

Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
355 360 365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
370 375 380

Gln Asp Xaa Pro Pro Xaa Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
385 390 395 400

Phe Xaa His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
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Lys Gly Asp Asp Tyr
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ctgtttccag atggaaagta cccagaaggt gcgtggatgg actatcatca agatttcaat 240
ctgcaaagaa ccacggatga agaatcacgt tatttggaaa gggatctgg aaggggccgaa 300
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<212> PRT

<213> Homo Sapiens

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<223> Human MetAP2

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35 40 45

Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
50 55 60

Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
65 70 75 80

Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Gln Tyr
325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
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Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
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Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
465 470 475

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<213> Mus musculus

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<223> Mouse MetAP2

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Met Ala Gly Val Glu Gln Ala Ala Ser Phe Gly Gly His Leu Asn Gly
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Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
35 40 45

Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
450 455 460

Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
465 470 475

<210> 14
<211> 437
<212> PRT
<213> *Saccharomyces* sp.

<220>
<223> Yeast MetAP2

<400> 14
Met Thr Asp Ala Glu Ile Glu Asn Ser Pro Ala Ser Asp Leu Lys Glu
1 5 10 15

Leu Asn Leu Glu Asn Glu Gly Val Glu Gln Gln Asp Gln Ala Lys Ala
20 25 30

Asp Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys
35 40 45

Lys Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp

50

55

60

Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
65 70 75 80

Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
85 90 95

Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
100 105 110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
115 120 125

Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
130 135 140

Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
145 150 155 160

Gly Phe Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala His Phe Thr
165 170 175

Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
180 185 190

Val Asp Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Asp Ser Ala Phe
195 200 205

Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
210 215 220

Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
225 230 235 240

Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
245 250 255

Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Leu Cys
260 265 270

Gly His Ser Ile Ala Pro Tyr Arg Ile His Gly Gly Lys Ser Val Pro
275 280 285

Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
290 295 300

Ala Ile Glu Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
305 310 315 320

Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
325 330 335

Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln

355

360

365

Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
370 375 380

Gln Asp Tyr Pro Pro Leu Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
385 390 395 400

Phe Glu His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
405 410 415

Lys Gly Asp Asp Tyr Gly Lys Met Arg Phe Gln Met Ala Ser Ser Leu
420 425 430

Gly Ile Ile Leu Leu
435

<210> 15

<211> 71

<212> PRT

<213> Rattus sp.

<220>

<223> Rat polylysine

<400> 15

Lys Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala Val Ser Ala
1 5 10 15

Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val Asp Glu Val
20 25 30

Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu Lys Asp Asp
35 40 45

Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala Gly Lys Lys
50 55 60

Lys Lys Lys Lys Lys Lys
65 70

<210> 16

<211> 480

<212> PRT

<213> Rattus sp.

<220>

-<223> Rat dnvMetAP2

<220>

<221> SITE

<222> (219)

<223> May be any naturally occurring amino acid

<220>

<221> SITE
<222> (231)
<223> May be any amino acid, except His

<220>
<221> SITE
<222> (251)
<223> May be any naturally occurring amino acid

<220>
<221> SITE
<222> (262)
<223> May be any naturally occurring amino acid

<220>
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<222> (328)
<223> May be any naturally occurring amino acid

<220>
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<222> (331)
<223> May be any naturally occurring amino acid

<220>
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<222> (338) .. (339)
<223> May be any naturally occurring amino acid

<220>
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<222> (364)
<223> May be any naturally occurring amino acid

<220>
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<222> (444)
<223> May be any naturally occurring amino acid

<220>
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<222> (447)
<223> May be any naturally occurring amino acid

<220>
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<222> (459)
<223> May be any naturally occurring amino acid

<400> 16
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1 5 10 15

Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
20 25 30

Glu Ala Ala Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala

35

40

45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
325 330 335

Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala

340

345

350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Cys
450 455 460

Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
465 470 475 480

<210> 17

<211> 480

<212> PRT

<213> Rattus sp.

<220>

<223> Rat MetAP2

<400> 17

Met Ala Gly Val Glu Glu Ala Ser Ser Phe Gly Gly His Leu Asn Arg
1 5 10 15

Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
20 25 30

Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
35 40 45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
50 55 60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
65 70 75 80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Ala Ala
85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
130 135 140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
165 170 175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
245 250 255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
260 265 270

Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
290 295 300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
340 345 350

Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
355 360 365

Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
370 375 380

Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
385 390 395 400

His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
405 410 415

Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Cys
450 455 460

Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
465 470 475 480

<210> 18
<211> 1944
<212> DNA
<213> Rattus sp.

<220>
<223> Rat MetAP2 variant

<220>
<221> misc_feature
<222> (779)
<223> Any nucleotide

<400> 18
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gccacctgaa tcgcgacctg gatccagacg acagggaaaga gggAACCTCC agcacggccg 180
aggaagccgc caagaagaaa agacggaaaga agaagaaggg caaaggggct gtgtcagcag 240
ggcaacaaga acttgataaa gaatcgaaa cctcagtggc cgaagttagca aaacagttgg 300
agagacaagc actggaggag aaagagaaaat atgatgacga tgaagatggc gatgggtatg 360
gtgatggtgc agctggaaag aagaagaaaa agaagaagaa gaagagagga ccaagagttc 420
aaacagaccc tccctcagtt ccaatatgtg acctgttatcc taatgggtgtta tttcccaaag 480
gacaagagtg tgaataccctt cccacccaaatgatggcgac agctgcttgg agaaccacaa 540
gtgaagagaaa aaaggcgcta gaccaggcta gtgaggagat ttggAACGAC ttcccgaaaag 600
ctgccaagc acaccggcaa gtttagaaat acgtcatgat ctggatcaag cctggatgt 660
caatgataga aatatgtgag aagttggaaag actgttccccaaagactctcata aaggagaatg 720
ggttaaatgc aggccctggcc tttcccactg ggtttctctt caacaactgt gctgcagcnt 780
acactcccaa tgctgggtgac acgacagtct tacagtacga cgacatctgt aagatcgact 840
ttggAACGCA tataagtggc tataataattt attgtgttt tactgttact ttaatccca 900
aatatgacat attattaaaaa gctgtaaaaatgatggcaccata tactggaaata aagtgtgcgg 960
ggattgacgt ccgtctctgt gatgtcgccg aggccattca agaagtatg gagtccat 1020
aagtggaaat agatggaaag acctaccaag tggaaacccat acgtaactta aatggacatt 1080
caattggggcc atatagaatt catgctggaa aaacagtggcc cattgtggaaa ggagggaaag 1140
ctacaaggat ggaggaagga gaggtgtatg ccattgagac ctttggtagc acagggaagg 1200
gcgtgggttca tgacgatatg gaatgttac actacatgaa aaattttgtat gtggggacacg 1260
tgccaataag gcttccaaga acaaaacact tggttgaatgt catcaatgaa aactttggta 1320
cccttgcctt ctgcccgaagg tggctggatc gcttggaga aagtaaatac ttaatggctc 1380
tgaagaacct gtgtgacttg ggcattgttag atccatatcc accactctgt gacattaaag 1440
gatcatacac acgacagtttt gaacatacca tactctgcgc ccaacctgtta aagaagtgt 1500
cagcagagga gatgactatt aaaacttagt ccaaagccaa ctcaacgtct ttatTTCTA 1560
agctttgttg gaacacatta taccacaagt aatttgcacatgtctgttt taacagtggta 1620
cctgtgtat ggcgttatcc atgtttaaag gagtttgatc aaagccaaac tgcgttacatg 1680
taattaaacca agggaaaaggc tttcaagact ttactgtttaa ctgtttctcc cgtcttaggaa 1740
atgctgtact gctcactagt taggaattac ttaaacgttt tggtttgaag acctaagaga 1800

tgcttttgg atatttatat tgccatattc ttacttggat gctttgaatg actacataca 1860
tccagttctg cacctatgcc ctctggatt gcttttaac cttcctggaa tccatTTCT 1920
aaaaaaaataaa gacatttca gatc 1944

<210> 19
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
transit peptide

<400> 19
Gly Arg Lys Lys Arg Arg Gln Arg
1 5

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20

gcgcagaGtt atgattgaat tactgtttcc agatggaaag 40

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21

gcgcctcgag tcagtagtca tcaccttcg aaacg 35

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 22

Cys Lys Glu Val Val Ser Lys Gly Asp Asp Tyr
1 5 10

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 23
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 24
Met Gly Met Met
1

<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
cacactcgac cgcgatgtac tactactact actactacta ctactacggg ccagatatac 60
gca 63

<210> 26
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
cacagaattc cccgcattccc cagcatgcct gctattg